High Throughput for High-resolution Cryo Electron Tomography

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Cryo-electron tomography (CryoET) and subtomogram averaging (STA), empowered by the rapid technological advancement in recent years, have turned into a very promising tool for high-resolution in-situ structural determination, opening a path to gain insight into the molecular mechanisms of cellular pathways. However, technological hurdles remain challenging for thick biological samples that have low-copy number of objects, demanding daunting numbers of tomograms for STA to make the critical yet faint high-resolution structures stand out. Our endeavors seek to significantly improve the throughputs for both tomographic data collection, alignment, and reconstruction. To this end, we propose a fully automated preprocessing pipeline that integrates MotionCor2 and AreTomo (www.msg.ucsf.edu/software) along with CTF estimation in a single application accelerated by multiple GPUs, enabling online generation of tomograms with all the needed meta data for STA. Our renewed effort on continuous tomography is also discussed to expedite the tomographic data collection.